

RAW SEQUENCE LISTING

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Application Serial Number: 10/553,124
Source: JFWO
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DATE: 08/25/2006

PATENT APPLICATION: US/10/553,124

TIME: 11:46:05

Input Set : A:\279689US0XPCT.ST25.txt

Output Set: N:\CRF4\08252006\J553124.raw

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3 <110> APPLICANT: ENDO, NOBORU
4      YOSHIDA, KOUKI
5      AKIYOSHI, MIHO
6      YOSHIDA, YASUKO
7      OHSUMI, CHIEKO
8      IGARASHI, DAISUKE
10 <120> TITLE OF INVENTION: GENE CAPABLE OF IMPARTING SALT STRESS RESISTANCE
12 <130> FILE REFERENCE: 279689US0XPCT
14 <140> CURRENT APPLICATION NUMBER: 10/553,124
15 <141> CURRENT FILING DATE: 2005-10-14
17 <150> PRIOR APPLICATION NUMBER: PCT/JP04/05403
18 <151> PRIOR FILING DATE: 2004-04-15
20 <150> PRIOR APPLICATION NUMBER: JP 2003-113194
21 <151> PRIOR FILING DATE: 2003-04-17
23 <150> PRIOR APPLICATION NUMBER: JP 2004-075932
24 <151> PRIOR FILING DATE: 2004-03-17
26 <160> NUMBER OF SEQ ID NOS: 17
28 <170> SOFTWARE: PatentIn version 3.3
30 <210> SEQ ID NO: 1
31 <211> LENGTH: 1554
32 <212> TYPE: DNA
33 <213> ORGANISM: Seashore Paspalum
36 <220> FEATURE:
37 <221> NAME/KEY: CDS
38 <222> LOCATION: (131)..(1222)
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43 acacgcccc tcgcgcgtc acacagagag agacacacag atcgatcgag cggccggccg      120
45 gacggcgcag atg gcg atc ggc ggg gcg gag gcc ggc ggg gga ggc gcg      169
46      Met Ala Ile Gly Gly Ala Glu Ala Gly Gly Gly Gly Ala
47      1              5              10
49 ggg gcc agc ggc cgg agc gtg ctg gtg acg ggc ggc gcg ggg ttc atc      217
50 Gly Ala Ser Gly Arg Ser Val Leu Val Thr Gly Gly Ala Gly Phe Ile
51      15              20              25
53 ggc acg cac acg gcg ctg cgc ctg ctg gag cag ggc tac ggc gtc acc      265
54 Gly Thr His Thr Ala Leu Arg Leu Leu Glu Gln Gly Tyr Gly Val Thr
55 30              35              40              45
57 gtc gtc gac aac ttc cac aac tcc gtc ccc gag gcg ctc gaa cgc gtc      313
58 Val Val Asp Asn Phe His Asn Ser Val Pro Glu Ala Leu Glu Arg Val
59      50              55              60
61 cgc ctc atc gcc ggg ccc gcg ctc tcc gcc cgc ctc gac ttc atc cgg      361
62 Arg Leu Ile Ala Gly Pro Ala Leu Ser Ala Arg Leu Asp Phe Ile Arg
63      65              70              75

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65	ggg gat ctg agg agc gcc ggg gac ttg gag aag gcg ttc gcg gcc agg	409
66	Gly Asp Leu Arg Ser Ala Gly Asp Leu Glu Lys Ala Phe Ala Ala Arg	
67	80 85 90	
69	agg tac gac gcc gtc gtc cac ttc gcg ggg ctc aag gcc gtc ggg gag	457
70	Arg Tyr Asp Ala Val Val His Phe Ala Gly Leu Lys Ala Val Gly Glu	
71	95 100 105	
73	agc gtc gcg cgc ccg gac atg tac tac gag aac aac ctc gcc ggc acc	505
74	Ser Val Ala Arg Pro Asp Met Tyr Tyr Glu Asn Asn Leu Ala Gly Thr	
75	110 115 120 125	
77	atc aac ctc tac aag gcc atg aac gag cac ggc tgc aag aag atg gtg	553
78	Ile Asn Leu Tyr Lys Ala Met Asn Glu His Gly Cys Lys Lys Met Val	
79	130 135 140	
81	ttc tcg tcg tcc gcg acc gtg tac ggc tgg ccg gag gtg atc ccg tgc	601
82	Phe Ser Ser Ser Ala Thr Val Tyr Gly Trp Pro Glu Val Ile Pro Cys	
83	145 150 155	
85	gtc gag gac tcc aag ctg cag gcc gcc aac ccc tac ggc agg acc aag	649
86	Val Glu Asp Ser Lys Leu Gln Ala Ala Asn Pro Tyr Gly Arg Thr Lys	
87	160 165 170	
89	ctc atc ctg gag gag ttg gcg cgg gac tac cag cgc gcg gac ccg ggc	697
90	Leu Ile Leu Glu Glu Leu Ala Arg Asp Tyr Gln Arg Ala Asp Pro Gly	
91	175 180 185	
93	tgg agc atc gtc ctg ctg cgc tac ttc aac ccc atc ggc gcc cac agc	745
94	Trp Ser Ile Val Leu Leu Arg Tyr Phe Asn Pro Ile Gly Ala His Ser	
95	190 195 200 205	
97	tcc ggc gag atc ggc gag gac ccc aag ggg gtg ccc aac aac ctg ctg	793
98	Ser Gly Glu Ile Gly Glu Asp Pro Lys Gly Val Pro Asn Asn Leu Leu	
99	210 215 220	
101	ccc tac atc cag cag gtc gcc gtc ggc agg ctc ccc gag ctc aac gtc	841
102	Pro Tyr Ile Gln Gln Val Ala Val Gly Arg Leu Pro Glu Leu Asn Val	
103	225 230 235	
105	tac ggc cac gat tac ccc acc cgt gac ggc acc gcg atc agg gac tac	889
106	Tyr Gly His Asp Tyr Pro Thr Arg Asp Gly Thr Ala Ile Arg Asp Tyr	
107	240 245 250	
109	ata cac gtc gtc gac ctg gcc gac ggg cac atc gcg gcg ctg aac aag	937
110	Ile His Val Val Asp Leu Ala Asp Gly His Ile Ala Ala Leu Asn Lys	
111	255 260 265	
113	ctg ttc gac act cct gat ttc ggt tgt gtg gcc tac aat ctg ggc aca	985
114	Leu Phe Asp Thr Pro Asp Phe Gly Cys Val Ala Tyr Asn Leu Gly Thr	
115	270 275 280 285	
117	ggg cgc ggc aca tcc gtt ctc gag atg gtg gcg gcg ttc aag aag gca	1033
118	Gly Arg Gly Thr Ser Val Leu Glu Met Val Ala Ala Phe Lys Lys Ala	
119	290 295 300	
121	tcc ggc aag gag atc ccc acc aag atg tgc ccc agg aga ccg ggt gac	1081
122	Ser Gly Lys Glu Ile Pro Thr Lys Met Cys Pro Arg Arg Pro Gly Asp	
123	305 310 315	
125	gcg acg gag gtt tac gcg tcc act gag aag gcc gaa agg gag ctc gga	1129
126	Ala Thr Glu Val Tyr Ala Ser Thr Glu Lys Ala Glu Arg Glu Leu Gly	
127	320 325 330	
129	tgg agg gcc cag tat gga atc gag gag atg tgc agg gac cag tgg aac	1177

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130 Trp Arg Ala Gln Tyr Gly Ile Glu Glu Met Cys Arg Asp Gln Trp Asn
131      335                      340                      345
133 tgg gcc aag aag aac ccc tat ggc tac tgc ggc act gcc gaa aaa      1222
134 Trp Ala Lys Lys Asn Pro Tyr Gly Tyr Cys Gly Thr Ala Glu Lys
135 350                      355                      360
137 tagagcgcgt gcattaatca gatctctgga ctgaatttgt ccatggttga tggttgtctc      1282
139 agacctatcg gtggaagatg taacaagtag agaccgctcg aatgtgccta gctacgaaag      1342
141 tttcgtacca tctctcttgt cataacctca tgtagatggg cattttattg gaattagcct      1402
143 tagccttcag gcccggcgct gttagccatt gcttgctatc gaggtaggtg gggttggaac      1462
145 tttgggcgcc cttgaacttc cattatcatc attcgcacag acggcacagt tgcgcagtga      1522
147 gccgttgact gcttgtgaaa aaaaaaaaaa aa      1554
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151 <211> LENGTH: 364
152 <212> TYPE: PRT
153 <213> ORGANISM: Seashore Paspalum
155 <400> SEQUENCE: 2
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158 1      5      10      15
161 Gly Arg Ser Val Leu Val Thr Gly Gly Ala Gly Phe Ile Gly Thr His
162      20      25      30
165 Thr Ala Leu Arg Leu Leu Glu Gln Gly Tyr Gly Val Thr Val Val Asp
166      35      40      45
169 Asn Phe His Asn Ser Val Pro Glu Ala Leu Glu Arg Val Arg Leu Ile
170      50      55      60
173 Ala Gly Pro Ala Leu Ser Ala Arg Leu Asp Phe Ile Arg Gly Asp Leu
174 65      70      75      80
177 Arg Ser Ala Gly Asp Leu Glu Lys Ala Phe Ala Ala Arg Arg Tyr Asp
178      85      90      95
181 Ala Val Val His Phe Ala Gly Leu Lys Ala Val Gly Glu Ser Val Ala
182      100     105     110
185 Arg Pro Asp Met Tyr Tyr Glu Asn Asn Leu Ala Gly Thr Ile Asn Leu
186      115     120     125
189 Tyr Lys Ala Met Asn Glu His Gly Cys Lys Lys Met Val Phe Ser Ser
190      130     135     140
193 Ser Ala Thr Val Tyr Gly Trp Pro Glu Val Ile Pro Cys Val Glu Asp
194 145     150     155     160
197 Ser Lys Leu Gln Ala Ala Asn Pro Tyr Gly Arg Thr Lys Leu Ile Leu
198      165     170     175
201 Glu Glu Leu Ala Arg Asp Tyr Gln Arg Ala Asp Pro Gly Trp Ser Ile
202      180     185     190
205 Val Leu Leu Arg Tyr Phe Asn Pro Ile Gly Ala His Ser Ser Gly Glu
206      195     200     205
209 Ile Gly Glu Asp Pro Lys Gly Val Pro Asn Asn Leu Leu Pro Tyr Ile
210      210     215     220
213 Gln Gln Val Ala Val Gly Arg Leu Pro Glu Leu Asn Val Tyr Gly His
214 225     230     235     240
217 Asp Tyr Pro Thr Arg Asp Gly Thr Ala Ile Arg Asp Tyr Ile His Val
218      245     250     255
221 Val Asp Leu Ala Asp Gly His Ile Ala Ala Leu Asn Lys Leu Phe Asp

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222          260          265          270
225 Thr Pro Asp Phe Gly Cys Val Ala Tyr Asn Leu Gly Thr Gly Arg Gly
226          275          280          285
229 Thr Ser Val Leu Glu Met Val Ala Ala Phe Lys Lys Ala Ser Gly Lys
230          290          295          300
233 Glu Ile Pro Thr Lys Met Cys Pro Arg Arg Pro Gly Asp Ala Thr Glu
234 305          310          315          320
237 Val Tyr Ala Ser Thr Glu Lys Ala Glu Arg Glu Leu Gly Trp Arg Ala
238          325          330          335
241 Gln Tyr Gly Ile Glu Glu Met Cys Arg Asp Gln Trp Asn Trp Ala Lys
242          340          345          350
245 Lys Asn Pro Tyr Gly Tyr Cys Gly Thr Ala Glu Lys
246          355          360
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250 <211> LENGTH: 23
251 <212> TYPE: DNA
252 <213> ORGANISM: Artificial Sequence
254 <220> FEATURE:
255 <223> OTHER INFORMATION: Synthetic DNA
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262 <211> LENGTH: 24
263 <212> TYPE: DNA
264 <213> ORGANISM: Artificial Sequence
266 <220> FEATURE:
267 <223> OTHER INFORMATION: Synthetic DNA
269 <400> SEQUENCE: 4
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273 <210> SEQ ID NO: 5
274 <211> LENGTH: 339
275 <212> TYPE: DNA
276 <213> ORGANISM: Artificial Sequence
278 <220> FEATURE:
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281 <400> SEQUENCE: 5
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284 ggacgccgag gaggccggcg gcgagaagaa gcaccacttc ttcggctgat ccatctcacc
286 atctccatct cccaccccca tcgatccatt tgtgttggct ttaattccct gcgtgcatgc
288 gtgttggtga ataaggggcc ggttccatct gtacgtacgt gtactccgag acctatcgtc
290 atgtgtgtgt gtgtacgtat acctgctgtg tacatgatgg tcgtatatgc cactggacta
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298 <213> ORGANISM: Seashore Paspalum
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305 ctcagaccta tcggtggaag atgtaacaag tagagaccgc tcgaatgtgc ctagctacga 180
307 agtttcgtac catctctctt gtcataacct catgtagatg gtcattttat tggaattagc 240
309 cttagccttc aggcccggcg ctgttaaaat ttgttttaca catggatttt ctcgctacgt 300
311 gtgatacata ttgtgtctgt aataatcctg atcggagttt ccagtaataa aaccgatcca 360
313 cgacggtggc tacgccctgt gttgtagtac tgtgaatatg atgtggtaat aacaataact 420
315 tgcagtgaga cttcagcttt caaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 480
317 aaaaaaaaaa aaaaaaa 497
320 <210> SEQ ID NO: 7
321 <211> LENGTH: 396
322 <212> TYPE: DNA
323 <213> ORGANISM: Artificial Sequence
325 <220> FEATURE:
326 <223> OTHER INFORMATION: Synthetic DNA
328 <400> SEQUENCE: 7
329 ggccgctgtg cagggaccag tggaactggg ccaagaagaa cccctatggc tactgcggca 60
331 ctgccgaaaa atagagcgcg tgcattaatc agatctctgg actgaatttg tccatgggtg 120
333 atggttgtct cagacctatc ggtggaagat gtaacaagta gagaccgctc gaatgtgcct 180
335 agctacgaag ttctgtacca tctctcttgt cataacctca tgtagatggc cattttattg 240
337 gaattagcct tagccttcag gcccggcgct gttaaaattt gttttacaca tggattttct 300
339 cgctacgtgt gatacatatt gtgtctgtaa taatcctgat cggagtttcc agtaataaaa 360
341 ccgatccacg acggtggcta cgccctgtgt tgtagt 396
344 <210> SEQ ID NO: 8
345 <211> LENGTH: 1540
346 <212> TYPE: DNA
347 <213> ORGANISM: Seashore Paspalum
350 <220> FEATURE:
351 <221> NAME/KEY: CDS
352 <222> LOCATION: (110)..(1183)
354 <400> SEQUENCE: 8
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358 Met Val Ser
359 1
361 gcg gtg ctt cgt acc atc ctt gtg acg ggc ggc gcc ggc tac atc ggc 166
362 Ala Val Leu Arg Thr Ile Leu Val Thr Gly Gly Ala Gly Tyr Ile Gly
363 5 10 15
365 agc cac acc gtg ctg ctg ctg ctg cag cag gga ttc cgc gtc gtc gtc 214
366 Ser His Thr Val Leu Leu Leu Leu Gln Gln Gly Phe Arg Val Val Val
367 20 25 30 35
369 gtc gac aac ctc gac aac gcc tcc gac gtc gcg ctc gcc cgc gtc gcg 262
370 Val Asp Asn Leu Asp Asn Ala Ser Asp Val Ala Leu Ala Arg Val Ala
371 40 45 50
373 cag ctc gca gca agc agc aac ggc ggc gcc gcc aac ctc gtc ttc cac 310
374 Gln Leu Ala Ala Ser Ser Asn Gly Gly Ala Ala Asn Leu Val Phe His
375 55 60 65
377 aag gtt gac ctt cgc gac agg cac gcg ctg gag gac atc ttc tcc tcc 358
378 Lys Val Asp Leu Arg Asp Arg His Ala Leu Glu Asp Ile Phe Ser Ser
379 70 75 80
381 cac agg ttt gag gct gtg att cat ttt gct ggg ctc aaa gct gtt ggc 406

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